

IN THE CLAIMS

Please amend the following claims as indicated below. A marked-up copy of all claims is attached for reference.

A1
3. (amended) Method according to claim 1, characterized in that the group I virus is selected from the group consisting of hordeiviruses, benyviruses, pecluviruses and pomoviruses, preferably selected from the group consisting of the beet necrotic yellow vein virus, the barley stripe mosaic virus, the potato mop top virus, the peanut clump virus and the beet soil-borne virus.

4. (amended) Method according to claim 1, characterized in that the plant cell is a stomatal cell.

5. (amended) Method according to claim 1, characterized in that the plant is selected from the group consisting of sugar beet, potato, barley or peanut.

6. (amended) Method according to claim 1, characterized in that the virus is BNYVV, the nucleotide sequence of TGB2 of said virus is comprised between the nucleotide 3287 and 3643 of the 5' strand of genomic or subgenomic RNA 2 of the BNYVV and the plant is a beet, preferably a sugar beet (*Beta vulgaris*).

7. (amended) Method according to claim 1, characterized in that the regulatory sequence comprises a promoter sequence or a terminator sequence active in a plant.

A2
10. (amended) Method according to claim 7, characterized in that the promoter sequence is a promoter which is capable of being active mainly into the root tissues of plants, such as the par promoter of the haemoglobin gene from *Perosponia andersonii*.

13. (amended) Transgenic plant according to claim 11, characterized in that the virus is selected from the group consisting of hordeiviruses, benyviruses, pecluviruses and pomoviruses, preferably selected from the group consisting of the beet necrotic yellow vein virus, the barley stripe mosaic virus, the potato mop top virus, the peanut clump virus and the beet soil-borne virus.

A3
14. (amended) Transgenic plant according to claim 11 being a plant selected from the group consisting of sugar beet, potato, barley or peanut.

15. (amended) Transgenic plant according to claim 11, characterized in that the transgenic plant being a beet, preferably a sugar beet (*Beta vulgaris*) the virus is BNYVV and the

nucleotide sequence of TGB2 of said virus is comprised between the nucleotides 3287 and 3643 of the 5' strand of genomic or subgenomic RNA 2 of BNYVV or its corresponding cDNA.

16. (amended) Transgenic plant according to claim 11, characterized in that the regulatory sequence comprises a promoter sequence and a terminator sequence active in a plant.

17. (amended) Transgenic plant according to claim 11, characterized in that the regulatory sequence(s) comprise a promoter sequence which is a constitutive or a foreign promoter sequence.

19. (amended) Transgenic plant according to claim 17, characterized in that the promoter sequence is a promoter which is capable of being active mainly into root tissues, such as the par promoter of the haemoglobin gene from *Perosponia andersonii*.

20. (amended) Transgenic plant according to claim 11, characterized in that it further carries natural tolerance to Group I viruses.

21. (amended) Transgenic plant according to claim 11, characterized in that it further comprises a pesticide, herbicide or fungicide resistance, preferably a resistance selected from the group consisting of nematode resistance, glyphosate resistance, glufosomate resistance and/or acetochloride resistance.

22. (amended) Transgenic plant tissue selected from the group consisting of fruit, stem, root, tuber, seed of a plant according to claim 11.

REMARKS

The above preliminary amendment is made to remove multiple dependencies from claims 3-7, 10, 13-17, 19-22, .

A new abstract page is supplied to conform to that appearing on the publication page of the WIPO application, but the new Abstract is typed on a separate page as required by U.S. practice.

Applicant respectfully requests that the preliminary amendment described herein be entered into the record prior to calculation of the filing fee and prior to examination and consideration of the above-identified application.